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## Technical note: Prediction of liveweight from linear conformation traits in dairy cattle

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### ABSTRACT

The objectives of this study were to derive phenotypic and genetic prediction equations of liveweight from linear conformation traits, and estimate genetic and phenotypic parameters for these traits. Data pertained to 2,728 conformation and liveweight records of 613 cows in 1,529 lactations. Cows were raised at the Scottish Agricultural College research station and had calved between 2002 and 2010. Fifteen linear conformation traits were considered as predictors. To validate phenotypic predictions, the data set was randomly split into independent reference and validation subsets. Reference subsets were used to derive prediction equations with the use of a mixed model. Comparisons between predicted and actual liveweight in the validation subsets indicated that stature, chest width, body depth, and angularity could be used to derive phenotypic predictions of liveweight. Accuracy of these predictions was better for first-lactation than for all-lactation liveweight data. Significant genetic correlations between liveweight and the 4 predictor traits ranged from 0.49 to 0.76, and phenotypic correlations were 0.33 to 0.56. Estimated genetic (co)variances were used to develop prediction equations of animal genetic merit for liveweight from routinely calculated genetic evaluations for conformation traits.

**Key words:** liveweight prediction, conformation trait

### Technical Note

Liveweight of a cow is routinely used as an on-farm monitoring and management tool (Maltz et al., 1997) and can be involved in the calculation of energy balance (Coffey et al., 2001). Energy costs associated with cow size are increasingly considered when estimating effectiveness and environmental impact of dairy production due to the association of dairy cow size with herd maintenance costs and efficiencies. To incorporate liveweight

into an overall selection index requires some way of routinely estimating it at the animal or sire level.

Banos and Coffey (2010) proposed a body energy content indicator based on body condition score and liveweight that could be used in genetic selection programs aiming at enhancing cow robustness. However, although body condition score is now routinely assessed in the commercial population in the UK and some other countries at the time of cow classification for linear conformation traits, liveweight records are missing from the national data. Because of the lack of accurate weighing scales at low cost, no large-scale recording of liveweight is anticipated in the near future, leaving prediction of liveweight from other nationally recorded traits as the only option.

Linear conformation traits have been used to predict liveweight at the phenotypic level (Koenen and Groen, 1998; Coffey et al., 2003). Equations derived from the work of Coffey et al. (2003) have been used to predict liveweight for management purposes in the UK. However, these equations were based on cow records from the 1990s, and the need for an update has arisen. Furthermore, the need exists to predict animal genetic merit for liveweight from their genetic evaluations for conformation traits to include liveweight into overall selection indices. The latter requires knowledge of the current genetic and phenotypic (co)variance matrix of liveweight and conformation traits.

The objectives of this study were to derive (1) phenotypic prediction equations of cow liveweight from linear conformation traits, (2) genetic and phenotypic (co) variance estimates for these traits, and (3) a formula to predict animal genetic merit for liveweight from genetic evaluations of conformation traits.

Data included 613 Holstein cows raised at the Scottish Agricultural College research station (Dumfries, Scotland) that had calved between 2002 and 2010. As part of ongoing selection and feeding experiments, cows belonged to a control or select genetic line as well as to a low or high concentrate diet group (Coffey et al., 2003).

Cows had multiple lactations for a total number of lactations equal to 1,529. Each cow was classified up to

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3 times during lactation by official classifiers of the Holstein UK breed society according to national specifications (Holstein UK, 2005). Fifteen linear conformation traits were scored during classification. A description of these traits is available at Holstein UK (2005). Cows were also weighed thrice daily, and the weekly average of all measurements on the week of classification was calculated to derive a weight record corresponding to the conformation records. The final data set comprised 2,728 weight records and conformation scores.

Subsequently, the data set was randomly split into 3 independent subsets, each including different animals. In 3 sequential permutations, 2 of the 3 subsets were merged into a reference subset, and the third was used as a validation subset. In each of the 3 permutations, a different validation subset was considered. Reference subsets were used to derive phenotypic prediction equations, which were then applied to the validation subsets to compare predicted with actual liveweight.

The following mixed model (model [1]) was used to derive phenotypic prediction equations for liveweight:

$$\text{LWT}_{ijklmnop} = \mu + Y_i + M_j + GG_k + FG_l + L_m + b \times \text{age} + \Sigma \beta_n \times x_n + \text{cow}_o + e_{ijklmnop}, \quad [1]$$

where  $\text{LWT}_{ijklmnop}$  = liveweight record,  $\mu$  = overall mean effect,  $Y_i$  = fixed effect of  $i$ th year of weight (8 classes),  $M_j$  = fixed effect of  $j$ th month of weight (12 classes),  $GG_k$  = fixed effect of  $k$ th genetic group (2 classes for control and selected animals),  $FG_l$  = fixed effect of  $l$ th diet group (2 classes for animals on low and high concentrate diets),  $L_m$  = fixed effect of  $m$ th lactation number (3 classes for first, second, and third or greater lactation),  $b$  = linear regression on age of cow at weighing (age),  $\beta_n$  = linear regression on  $n$ th conformation trait ( $x_n$ ) summed over all conformation traits,  $\text{cow}_o$  = random effect of  $o$ th cow, and  $e_{ijklmnop}$  = random residual effect.

Fixed effects in model [1] were determined in a series of preliminary analyses in which the effect of various factors on liveweight was assessed. Factors included in model [1] were those with the highest significant effect on liveweight. Furthermore, this model was associated with the best fit, as assessed by the comparison between predicted and actual liveweight described later. Two sets of analyses were conducted using either first-lactation data only or all-lactation data. In the first-lactation data analysis, the effect of lactation was not included in model [1].

In all cases, model [1] was first applied to the entire data set, fitting one conformation trait at a time. Subsequently, model [1] was fitted to the reference

subsets starting with the conformation trait with the largest individual  $F$ -value and then fitting sequentially additional traits according to their  $F$ -values. Solutions were then applied to the validation subsets using the following formula:

$$\text{LWT} = \text{constant} + L + b \times \text{age} + \Sigma \beta \times x,$$

where LWT = predicted liveweight phenotype of cow, constant = sum of solution of the overall mean effect and average solutions of year and month of weight/classification, and genetic and diet group,  $L$  = solution of the corresponding lactation, when applicable,  $b$  = estimate of slope of regression on age of cow at weighing (age), and  $\beta$  = estimate of slope of regression on conformation trait ( $x$ ) summed over all conformation traits.

Predicted liveweight was compared with the actual liveweight in the validation subsets. Comparison criteria included the average absolute difference, root mean square error, and product-moment correlation. (Co) variance estimates between liveweight and conformation traits were calculated with a multivariate model that included effects similar to the UK national genetic evaluation model for conformation traits (Brotherstone et al., 1990). Thus, year-season of inspection, age of cow at inspection (linear regression), stage of lactation at inspection (linear and quadratic regression), and month of calving were fitted as fixed effects. In addition, the model included the fixed effects of diet and genetic group that were specific to this data set. Cow and permanent environment were fitted as random effects. Variance heterogeneity among classifiers was accounted for by pre-adjusting conformation scores by the ratio of the overall standard deviation to classifier standard deviation; this is the routine practice in the UK national genetic evaluation system (Brotherstone et al., 1990). A pedigree relationship matrix comprising 2,308 individual animals was included in the analysis to distinguish genetic from environmental effects.

Genetic (co)variance estimates from the multivariate analysis were used to derive the following prediction formula of animal genetic merit for liveweight from EBV for conformation traits:

$$\text{EBV}_{\text{LWT}} = \mathbf{G}_{\text{LWT,C}}' \mathbf{G}_{\text{CC}}^{-1} \mathbf{EBV}_{\text{C}},$$

where  $\text{EBV}_{\text{LWT}}$  = predicted animal genetic merit for liveweight,  $\mathbf{G}_{\text{LWT,C}}$  = vector of genetic covariance estimates of liveweight with conformation traits,  $\mathbf{G}_{\text{CC}}$  = matrix of the genetic (co)variance estimates of conformation traits, and  $\mathbf{EBV}_{\text{C}}$  = vector of animal EBV for conformation traits.

**Table 1.** Wald statistic ( $F$ -value) and associated  $P$ -value of the effect of each conformation trait fitted individually on liveweight

Trait	First lactation		All lactations	
	$F$ -value	$P$ -value	$F$ -value	$P$ -value
Chest width	256.93	0.00	671.25	0.00
Stature	109.83	0.00	212.25	0.00
Body depth	93.36	0.00	272.43	0.00
Angularity	13.04	0.00	81.09	0.00
Central ligament	9.48	0.00	6.56	0.01
Udder depth	5.87	0.02	6.35	0.01
Foot angle	5.51	0.02	21.86	0.00
Teat length	2.41	0.12	1.90	0.17
Rump width	1.91	0.17	7.89	0.01
Fore udder attachment	1.73	0.19	58.67	0.00
Rump angle	1.58	0.21	6.69	0.01
Rear teat position	1.26	0.26	5.90	0.02
Rear leg side view	1.24	0.27	0.75	0.39
Teat position side	0.29	0.59	5.99	0.01
Rear udder height	0.00	1.00	11.01	0.00

The above formula is based on the theory of Henderson (1977) and was used by Mark et al. (2007) to predict breeding values for missing traits based on their genetic correlation with available traits in international genetic evaluations.

Table 1 summarizes results from fitting each conformation trait separately in the model. For first lactation, chest width, stature, body depth, angularity, central ligament, udder depth, and foot angle were associated with significant ( $P < 0.05$ ) individual  $F$ -values. When all lactations were considered, the only traits without a significant effect on liveweight were teat length and rear leg side view. In both analyses, the 4 traits with the greatest individual effect were stature, chest width, body depth, and angularity. These traits relate to the volume of the trunk of the cow body, and the same traits were found to have the most significant effect on liveweight in the study of Coffey et al. (2003).

Results of the comparison between actual and predicted liveweight from traits with significant ( $P < 0.05$ ) individual  $F$ -values are shown in Table 2 (first-lactation data) and Table 3 (all-lactation data). These results are the averages of 3 permutations. In each case, traits

were added stepwise according to their  $F$ -value (Table 1), starting with the trait with the largest individual  $F$ -value (chest width). In both cases, the predictive capacity of the model, assessed by the average absolute difference, root mean square error, and product-moment correlation, improved substantially until all 4 top traits (chest width, stature, body depth, and angularity) were included. It should be noted that lower absolute differences and root mean square errors and high correlation estimates are associated with an improved fit of the model. No further improvements were observed from adding more traits in the analysis of first-lactation data. Inclusion of more than one trait, in addition to the top 4, in the model did not improve the fit.

Based on these results, stature, chest width, body depth, and angularity are proposed as predictor traits for the phenotypic prediction of liveweight. Coffey et al. (2003) considered the same 4 predictor traits in their study of earlier data from the same herd. Average absolute difference and root mean square error associated with predictions in the present study were 5.0 and 6.5% of mean first-lactation liveweight and 15.2 and 17.6% of mean all-lactation liveweight, respectively. As expected,

**Table 2.** Average absolute difference (AbsDiff), root mean square error (RMSE), and product-moment correlation (Corr) between actual and predicted liveweight from linear conformation traits (first-lactation data)

Conformation traits in prediction model	AbsDiff	RMSE	Corr
Chest width	33.22	43.01	0.75
Chest width + stature	30.05	38.78	0.80
Chest width + stature + body depth	29.91	38.09	0.81
Chest width + stature + body depth + angularity	28.67	36.74	0.83
Chest width + stature + body depth + angularity + central ligament	28.80	36.75	0.83
Chest width + stature + body depth + angularity + udder depth	28.80	36.80	0.82
Chest width + stature + body depth + angularity + foot angle	28.73	36.71	0.83
All above traits	28.70	36.55	0.83
All 15 conformation traits	29.05	36.69	0.82

**Table 3.** Average absolute difference (AbsDiff), root mean square error (RMSE), and product-moment correlation (Corr) between actual and predicted liveweight from linear conformation traits (all-lactation data)

Conformation traits in prediction model	AbsDiff	RMSE	Corr
Chest width	112.07	127.91	0.70
Chest width + body depth	103.78	120.16	0.74
Chest width + body depth + stature	93.66	108.85	0.79
Chest width + body depth + stature + angularity	91.03	105.38	0.81
Chest width + body depth + stature + angularity + fore udder attachment	93.44	108.14	0.80
Chest width + body depth + stature + angularity + foot angle	92.69	107.05	0.80
Chest width + body depth + stature + angularity + rear udder height	90.40	104.82	0.81
Chest width + body depth + stature + angularity + rump width	91.22	105.63	0.81
Chest width + body depth + stature + angularity + rump angle	90.93	105.13	0.81
Chest width + body depth + stature + angularity + central ligament	91.98	106.42	0.80
Chest width + body depth + stature + angularity + udder depth	95.79	110.39	0.79
Chest width + body depth + stature + angularity + teat position side	91.29	105.63	0.81
Chest width + body depth + stature + angularity + rear teat position	92.07	106.40	0.81
All above traits	92.53	107.32	0.79
All 15 conformation traits	95.23	110.13	0.78

predictions were more accurate in first lactation when more data were available and the variation of liveweight was smaller. Previous similar studies (Koenen and Groen, 1998; Coffey et al., 2003) considered only first-lactation data. Final phenotypic prediction equations derived in the present study are shown below:

First-lactation data:

$$\text{LWT} = 239.66 + 7.111 \times \text{age} + 9.865 \times \text{Sta} \\ + 9.055 \times \text{CW} + 5.974 \times \text{BD} - 5.132 \times \text{Ang}.$$

All-lactation data:

$$\text{LWT} = 398.72 + 1.926 \times \text{age} + 10.55 \times \text{Sta} \\ + 9.432 \times \text{CW} + 8.551 \times \text{BD} - 7.822 \times \text{Ang} + \text{L},$$

where LWT = predicted liveweight (kg), age = age of cow at classification (mo), Sta = stature (1–9), CW = chest width (1–9), BD = body depth (1–9), Ang = angularity (1–9), and L = 0 for first, 24.41 for second, and 23.75 for third or later lactations.

Because the constant term in the above equations includes the solution of the overall mean effect and the average solutions of year and month of weight and genetic and diet group, equation coefficients were considered to be adjusted for these effects and applicable to other data sets, too.

First-lactation coefficients were in the same range as those reported by Coffey et al. (2003), who used older data from the same herd. Corresponding coefficients in the study of Coffey et al. (2003) were 8.529, 8.505, 5.548, and  $-7.247$  for stature, chest width, body depth, and angularity, respectively.

Heritability and genetic and phenotypic correlation estimates of liveweight and the 4 predictor conforma-

tion traits are shown in Table 4 (first-lactation data) and Table 5 (all-lactation data). Liveweight had a significant ( $P < 0.05$ ) positive genetic correlation with stature, chest width, and body depth (all-lactation data). This is consistent with first-lactation estimates reported by Koenen and Groen (1998) for Dutch cattle and multiple lactation estimates reported by Vallimont et al. (2010) for US cattle. Specifically, genetic correlations of BW with body depth and size (a trait similar to stature) in the study of Koenen and Groen (1998) were 0.48 and 0.59, respectively. Vallimont et al. (2010) reported genetic correlations of BW with body depth and stature equal to 0.57 and 0.94, respectively. Vallimont et al. (2010) also reported a nonsignificant correlation with dairy form, which is consistent with the results for angularity found in the present study.

Similarly, significant ( $P < 0.05$ ) positive phenotypic correlations were observed between liveweight and stature, chest width, and body depth. A significant ( $P < 0.05$ ) negative phenotypic correlation was found between liveweight and angularity. The signs of these phenotypic correlations are consistent with the signs of the slope estimates in the phenotypic prediction equations presented above. These estimates are similar to the findings of Koenen and Groen (1998), who reported phenotypic correlations of first-lactation BW with body depth and size equal to 0.42 and 0.49, respectively. Furthermore, estimates from the all-lactation data were similar to those of Vallimont et al. (2010), who reported 0.32, 0.38, and  $-0.10$  for body depth, stature, and dairy form, respectively.

These parameter estimates were derived from (co) variance components of the 5-trait analysis. Genetic (co)variance estimates from this analysis were used to derive prediction equations of animal genetic merit for liveweight from genetic evaluations for conformation traits.



**Table 4.** Heritability (diagonal) and genetic (below diagonal) and phenotypic (above diagonal) correlation estimated for first-lactation data; estimates were significantly different from zero ( $P < 0.05$ ) unless otherwise indicated

	Liveweight	Stature	Chest width	Body depth	Angularity
Liveweight	0.38	0.49	0.56	0.33	-0.08
Stature	0.56	0.34	0.15	0.35	0.21
Chest width	0.76	0.06 <sup>NS</sup>	0.22	0.28	-0.10
Body depth	0.27 <sup>NS</sup>	0.45	0.28 <sup>NS</sup>	0.23	0.55
Angularity	-0.27 <sup>NS</sup>	0.22 <sup>NS</sup>	-0.29 <sup>NS</sup>	0.80	0.12

NS:  $P > 0.05$ .

Genetic covariance estimates of liveweight with conformation traits (stature, chest width, body depth, and angularity, respectively) were 10.890, 14.618, 5.666, and -4.108 for first-lactation data and 15.996, 15.689, 14.267, and 0.584 for all-lactation data.

Genetic (co)variance matrices among the 4 conformation traits (stature, chest width, body depth, and angularity, respectively) were 0.494, 0.030, 0.234, 0.085, 0.030, 0.484, 0.146, -0.110, 0.234, 0.146, 0.553, 0.327, 0.085, -0.110, 0.327, 0.301 for first-lactation data and 0.579, 0.088, 0.398, 0.161, 0.088, 0.439, 0.272, -0.014, 0.398, 0.272, 0.794, 0.351, 0.161, -0.014, 0.351, 0.273 for all-lactation data.

Multiplying the genetic covariance vector by the inverse of the genetic (co)variance matrix yielded the coefficients of the genetic prediction equation as follows:

First-lactation data:

$$\text{EBV}_{\text{LWT}} = 22.843 \times \text{EBV}_{\text{Sta}} + 27.998 \times \text{EBV}_{\text{CW}} - 2.616 \times \text{EBV}_{\text{BD}} - 7.078 \times \text{EBV}_{\text{Ang}},$$

All-lactation data:

$$\text{EBV}_{\text{LWT}} = 26.917 \times \text{EBV}_{\text{Sta}} + 31.284 \times \text{EBV}_{\text{CW}} - 1.983 \times \text{EBV}_{\text{BD}} - 9.620 \times \text{EBV}_{\text{Ang}},$$

where  $\text{EBV}_{\text{LWT}}$  = predicted genetic merit for liveweight,  $\text{EBV}_{\text{Sta}}$  = EBV for stature,  $\text{EBV}_{\text{CW}}$  = EBV for chest width,  $\text{EBV}_{\text{BD}}$  = EBV for body depth, and  $\text{EBV}_{\text{Ang}}$  = EBV for angularity.

The above equations assume high reliability of the EBV for conformation traits. One way to expand their utility would be to weigh each EBV by their reliability. This, however, would diminish the size of the equation coefficients, effectively regressing the predicted genetic merit for liveweight toward the mean. Therefore, it is recommended to apply these equations only to official genetic evaluations with a minimum reliability that meets publication requirements.

Although the genetic correlation between liveweight and angularity was not different from zero (Tables 3 and 4), the latter was included in the genetic prediction equations for consistency with the phenotypic prediction equations described previously in this paper.

Prediction of genetic merit for liveweight would be of particular importance to imported sires whose daughters' classification records are not available to phenotypically predict liveweight and calculate genetic evaluations. Interbull genetic evaluations for conformation traits may be directly used to predict genetic merit for liveweight in various countries. In practice, genetic evaluations for conformation traits around the world are based on first-lactation data. Therefore, the first-lactation equations developed in this study are considered the most useful and are recommended for implementation.

Coefficients derived in the present study were based on a single cow population. Validation in other herds and populations would be desirable. Furthermore, phenotypic and genetic (co)variance matrices from the present study could also be used to derive weights for including predicted liveweight in a selection index. The

**Table 5.** Heritability (diagonal) and genetic (below diagonal) and phenotypic (above diagonal) correlation estimated for all-lactation data; estimates were significantly different from zero ( $P < 0.05$ ) unless otherwise indicated

	Liveweight	Stature	Chest width	Body depth	Angularity
Liveweight	0.41	0.49	0.53	0.35	-0.08
Stature	0.65	0.42	0.14	0.37	0.23
Chest width	0.73	0.17 <sup>NS</sup>	0.21	0.30	-0.12
Body depth	0.49	0.59	0.46	0.32	0.52
Angularity	0.03 <sup>NS</sup>	0.40	-0.04 <sup>NS</sup>	0.75	0.13

NS:  $P > 0.05$ .

expected response to selection on this index of the 4 linear conformation traits will need to be investigated. At either the phenotypic or genetic merit level, predicted liveweight can be a first step in the process of including some measure of energy use efficiency in dairy cattle breeding indices based on field data. The energy cost of liveweight will need to be determined in this regard.

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